

REMARKS**Claim Amendments**

Claims 29, 31, 33-34, 37-41, and 43-47 are canceled without prejudice or disclaimer. Claims 25-28, 32 and 35 remain pending. Claim 25 is amended to recite “a method of eliciting a Chlamydia specific immune response in a patient” and “serovar homologue.” No new matter is added by these claim amendments. See, for example, page 9, lines 18-20 of the specification.

Entry of this Amendment is respectfully requested because the response (1) does not raise any new issues, (2) places this application in condition for allowance, and/or (3) simplifies the issues for appeal.

Claim objection

Claim 37 was objected to for a misspelled word. Claims 25 and 37 were objected to for improper Markush claim language. Claim 25 has been amended accordingly. Claim 37 is canceled. Withdrawal of the objection is respectfully requested.

The Rejection of Claims 25-29, 31-35, 37-41, and 43-47 Under 35 U.S.C. § 112, First Paragraph

Claims 25-29, 31-35, 37-41, and 43-47 were rejected under 35 U.S.C. § 112, first paragraph as allegedly failing to provide an adequate written description and enablement. The Office Action asserts that although the specification provides adequate support for the immunogenicity of ribosomal L7/L12, ribosomal L7/L12 protein is allegedly not disclosed as treating or preventing Chlamydia infection. Claims 37-41 and 43-47 have

been canceled. Claim 25 (and dependent claims 26-29 and 31-35), as amended, is directed to a method of eliciting a Chlamydia specific immune response in a patient. The Office Action admits that the specification provides adequate support for eliciting an immune response. Indeed, the specification discloses at page 12, lines 10-12, “seven patients show reactivity to this [ribosomal protein L7/L12] protein, demonstrating that it is immunogenic in humans as a consequence of chlamydial infection” and also discloses at page 8, lines 19-22, “patient immune reactions were also detected against the following proteins: ... spot 12 – ribosomal protein L7/L12 (7/17)”. The specification also at page 12, lines 27 to page 13, line 1, discloses “it is noteworthy that several of these new immunoreactive antigens belong to conserved families of bacterial proteins: ... seven sera (41%) recognised [sic] spot 12 (the ribosomal protein L7/L12).”

The Office Action further asserts that the specification allegedly fails to provide an enabling disclosure for a homologue of ribosomal protein L7/L12, a homologue which has greater than 50% identity to ribosomal protein L7/L12, a homologue with greater than 90% identity to ribosomal protein L7/L12 or fragments of ribosomal protein L7/L12 with at least 7 amino acids. Claim 1, as amended, is directed to subject matter which is fully supported by the specification. Therefore, withdrawal of the rejection is respectfully requested.

The specification discloses that the *C. trachomatis* serovar L2 strain was used in obtaining protein samples for immunoblot analysis (page 5, line 28 – page 6, line 3) and the N-terminal sequence data from the proteins was searched in a database for the CT D/UW-3/Cx strain (specification, page 9). The specification further discloses at page 9, lines 17-20 that “although the present study used a *C.trachomatis* serovar L2 strain

(lymphogranuloma biovar), which has a different pathogenicity phenotype, several protein sequences could be safely correlated to the serovar D genes.” Thus, the specification provides a written description of serovar homologues that would enable one of skill in the art to practice the invention without undue experimentation. Withdrawal of the rejection is respectfully requested.

The Rejection of Claims 25-29, 31-35, 37-41, and 43-47 Under 35 U.S.C. § 112, Second Paragraph

Claims 25-29, 31-35, 37-41, and 43-47 were rejected under 35 U.S.C. § 112, second paragraph as allegedly being indefinite for recitation of “Chlamydia ribosomal protein L7/L12.” The Office Action asserts that “[i]t appears that ‘L7 and L12’ is a lab[oratory] designation for this protein” and that terminology changes “from lab[oratory] to lab[oratory]”. However, contrary to the Office Action’s assertions, the designation “L7/L12” is recognized in the art. Indeed, the specification discloses ribosomal protein L7/L12 (spot 12) as a known protein (see specification, page 8, lines 22-23). Table 1 from Nature Genetics, Vol. 21, April 1999 is entitled “Functional Assignments of C. Pneumoniae coding sequences; C. trachomatis genes are shown in parentheses.” That table includes the L7/L12 ribosomal protein encoded by the r17 gene (see page 4, col. 2, under the heading “Ribosomal Proteins”). Also, the PubMed status report for Read et al, “Genome Sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39”, *Nucleic Acids Res.*, 28(6), 1397-1406 (2000) describes the 50S ribosomal protein L7/L12. Also, Engel et al, “cloning and Characterization of RNA polymerase core subunits of Chlamydia trachomatis by using the polymerase chain reaction”, *J. Bacteriol.* 172(10), 5732-5741 (1990) describes the L12P family of ribosomal proteins. A reference

previously cited on an Information Disclosure Statement also discusses the L7/L12 proteins (e.g., Sanchez-Campillo et al., *Electrophoresis* 20:2269-2279, 1999). The ribosomal protein L7/L12 is indeed recognized in the art as the specification states. Withdrawal of the rejection is respectfully requested.

Claims 25 and 37 were rejected under 35 U.S.C. § 112, second paragraph as allegedly being indefinite under the presumption that “L7/L12” is an abbreviation. As set forth above, “L7/L12” is not an abbreviation. Therefore, withdrawal of the rejection is respectfully requested.

Claims 27, 35, 39, and 47 were rejected under 35 U.S.C. § 112, second paragraph as allegedly being indefinite for recitation of “MW of about 15.8 kD.” Specifically, the Office Action asserts that the method by which a molecular weight was obtained should be provided. Pointedly, the specification discloses the methods employed in obtaining the molecular weights. For example, the specification at pages 6-7 discloses separation of chlamydial proteins using 2D electrophoresis, immunoblot analysis (Towbin et al (1979) – ref. 18), matching the immunoblot with a reference map and identifying MW and pI coordinates. Claims are not interpreted in a vacuum but rather should be construed in light of the specification (*Ex parte Kotler*, 1901 C.D. 62, 95 O.G. 2684 (Comm’r Pat. 1901). Withdrawal of the rejection is respectfully requested.

Applicants respectfully submit that the instant application is in condition for allowance. If the Examiner feels, however, that further discussion may be helpful in facilitating prosecution of the case, the Examiner is respectfully requested to telephone the undersigned attorney of record at the number appearing below.

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Respectfully submitted,

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Table 1 • Functional assignments of *C. Pneumoniae* coding sequences; *C. trachomatis* genes are shown in parentheses

Amino Acid Biosynthesis					
Aromatic Family			0871 (CT730)	ribD	Riboflavin Deaminase
1039 (CT366)	aroA	Phosphoshikimate Vinyltransferase	0873 (CT732)	ribE	Ribityllumazine Synthase
1036 (CT369)	aroB	Dehydroquinase Synthase	0320 (CT093)	ribF	FAD Synthase
1037 (CT368)	aroC	Chorismate Synthase	Cell Envelope		
1035 (CT370)	aroE	Shikimate 5-Dehydrogenase	Fatty Acid & Phospholipid Metabolism		
0484 (CT382)	aroG	Deoxyheptonate Aldolase	0161 (CT206)		(predicted acyltransferase family)
1038 (CT367)	aroL	Shikimate Kinase II	0922 (CT776)	aas	Acylglycerophosphoethanolamine Acyltransferase
0740 (CT637)	tyrB	Aromatic AA Aminotransferase	0414 (CT265)	accA	AcCoA Carboxylase/Transferase Alpha
Aspartate Family (lysine)			0183 (CT123)	accB	Biotin Carboxyl Carrier Protein
1048 (CT363)	asd	Aspartate Dehydrogenase	0182 (CT124)	accC	Biotin Carboxylase
1050 (CT361)	dapA	Dihydrodipicolinate Synthase	0058 (CT293)	accD	AcCoA Carboxylase/Transferase Beta
1047 (CT364)	dapB	Dihydrodipicolinate Reductase	0295 (CT236)	acpP	Acyl Carrier Protein
0519 (CT430)	dapF	Diaminopimelate Epimerase	0313 (CT100)	acpS	Acyl-carrier Protein Synthase
1049 (CT362)	lysC	Aspartokinase III	0567 (CT451)	cdsA	Phosphatidate Cytidylyltransferase
Serine Family			0297 (CT238)	fabD	Malonyl Acyl Carrier Transcyclase
0433 (CT282)	gcsH	Glycine Cleavage System H Protein	0916 (CT770)	fabF	Acyl Carrier Protein Synthase
0521 (CT432)	glyA	Serine Hydroxymethyltransferase	0296 (CT237)	fabG	Oxoacyl (Carrier Protein) Reductase
Base & Nucleotide Metabolism			0298 (CT239)	fabH	Oxoacyl Carrier Protein Synthase III
0171	guaA	GMP Synthase	0406 (CT104)	fabI	Enoyl-Acyl-Carrier Protein Reductase
0172	guaB	Inosine 5'-Monophosphate Dehydrogenase	0651 (CT532)	fabZ	Myristoyl-Acyl Carrier Dehydratase
0608		Uridine 5'-Monophosphate Synthase	0098 (CT010)	htrB	Acyltransferase
0735		Uridine Kinase	0271 (CT136)		Lysophospholipase Esterase
0244 (CT128)	adk	Adenylate Kinase	0615 (CT496)	pgsA_1	Glycerol-3-P Phosphatidyltransferase_1
0894 (CT751)	amn	AMP Nucleosidase	0947 (CT797)	pgsA_2	Glycerol-3-P Phosphatidyltransferase_2
0568 (CT452)	cmk	CMP Kinase	0958 (CT807)	plsB	Glycerol-3-P Acyltransferase
0392 (CT039)	dcd	dCTP Deaminase	0569 (CT453)	plsC	Glycerol-3-P Acyltransferase
0059 (CT292)	dut	dUTP Nucleotidohydrolase	0962 (CT811)	plsX	FA/Phospholipid Synthesis Protein
0120 (CT030)	gmk	GMP Kinase	0839 (CT699)	psdD	Phosphatidylserine Decarboxylase
0619 (CT500)	ndk	Nucleoside-2-P Kinase	0983 (CT826)	pssA	Glycerol-Serine Phosphatidyltransferase
0984 (CT827)	nrdA	Ribonucleoside Reductase, Large Chain	0921 (CT775)	snGlycerol-3-P	Acyltransferase
0985 (CT828)	nrdB	Ribonucleoside Reductase, Small Chain	0654 (CT535)	yciA	Acyl-CoA Thioesterase
0236 (CT183)	pyrG	CTP Synthetase	0877 (CT736)	ybcL	CT736 Hypothetical Protein
0698 (CT678)	pyrH	UMP Kinase	LPS		
0273 (CT188)	tdk	Thymidylate Kinase	0154 (CT208)	gseA	KDO Transferase
0659 (CT539)	trxA	Thioredoxin	0721 (CT655)	kdsA	KDO Synthetase
0314 (CT099)	trxB	Thioredoxin Reductase	0235 (CT182)	kdsB	Deoxyoctulononic Acid Synthetase
1001 (CT844)	yfhC	Cytosine Deaminase	0650 (CT531)	lpxA	Acyl-Carrier UDP-GlcNAc O-Acyltransferase
Biosynthesis of Cofactors			0965 (CT411)	lpxB	Lipid A Disaccharide Synthase
Biotin, Lipote & Ubiquinone			0652 (CT533)	lpxC	Myristoyl GlcNAc Deacetylase
1041	bioA	Adenosylmethionine-8-Amino-7-Oxononanoate Aminotransferase	0302 (CT243)	lpxD	UDP Glucosamine N-Acyltransferase
1044	bioB	Biotin Synthase	Membrane Proteins, Lipoproteins & Porins		
1042	bioD	Dethiobiotin Synthetase	0310 (CT251)	60IM	60kDa Inner Membrane Protein
0923 (CT777)	bioF_1	Oxononanoate Synthase_1	0556 (CT442)	crpA	15kDa Cysteine-Rich Protein
1043 (CT777)	bioF_2	Oxononanoate Synthase_2	0653 (CT534)	cutE	Apolipoprotein N-Acetyltransferase
0866 (CT725)	birA	Biotin Synthetase	0311 (CT252)	lgt	Prolipoprotein Diacylglycerol Transferase
0748 (CT628)	ispA	Geranyl Transferase	0558 (CT444)	omcA	9kDa-Cysteine-Rich Lipoprotein
0832 (CT558)	lipA	Lipote Synthetase	0557 (CT443)	omcB	60kDa Cysteine-Rich OMP
0265 (CT219)	ubiA	Benzoate Octaphenyltransferase	0695 (CT681)	ompA	Major Outer Membrane Protein
0264 (CT220)	ubiD	Phenylacrylate Decarboxylase	0854 (CT713)	ompB	Outer Membrane Protein B
0515 (CT428)	ubiE	Ubiquinone Methyltransferase	0781 (CT600)	pal	Peptidoglycan-Associated Lipoprotein
Folic Acid			0300 (CT241)	yaeT	Omp85 Homolog
0759 (CT612)	folA	Dihydrofolate Reductase	Peptidoglycan		
0335 (CT078)	folD	Methylene Tetrahydrofolate Dehydrogenase	0417 (CT268)	amiA	N-Acetylmuramoyl Alanine Amidase
0758 (CT613)	folP	Dihydropteroate Synthase	0780 (CT601)	amiB	N-Acetylmuramoyl-L-Ala Amidase
0757 (CT614)	folX	Dihydropteridine Aldolase	0672 (CT551)	dacF	D-Ala-D-Ala Carboxypeptidase
0763 (CT649)	ygfA	Formyltetrahydrofolate Cycloligase	0968 (CT816)	glmS	Glucosamine-Fructose-6-P Aminotransferase
Porphyrin			0749 (CT629)	glmU	UDP-GlcNAc Pyrophosphorylase
0714 (CT662)	hemA	Glutamyl tRNA Reductase	0900 (CT757)	mraY	Muramoyl-Pentapeptide Transferase
0744 (CT633)	hemB	Porphobilinogen Synthase	0571 (CT455)	murA	UDP-N-Acetylglucosamine Transferase
0052 (CT299)	hemC	Porphobilinogen Deaminase	0988 (CT831)	murB	UDP-N-Acetylenolpyruvoylglucosamine Reductase
0890 (CT747)	hemE	Uroporphyrinogen Decarboxylase	0905 (CT762)	murC	Muramate-Ala Ligase & D-Ala-D-Ala Ligase
0888 (CT745)	hemG	protoporphyrinogen Oxidase	0901 (CT758)	murD	Muramoylalanine-Glutamate Ligase
0138 (CT210)	hemL	Glutamate-1-Semialdehyde-2,1-Aminomutase	0418 (CT269)	murE	N-Acetylmuramoylalanineglutamate DAP Ligase
0380 (CT052)	hemN_1	Coproporphyrinogen III Oxidase_1	0899 (CT756)	murF	Muramoyl-DAP Ligase
0889 (CT746)	hemN_2	Coproporphyrinogen III Oxidase_2	0904 (CT761)	murG	Peptidoglycan Transferase
0603 (CT485)	hemZ	Ferrochelatase	0902 (CT759)	nlpD	Muramidase (invasin repeat family)
Riboflavin			0694 (CT682)	pbp2	PBP2-Transglycolase/Transpeptidase
0872 (CT731)	ribA&ribB	GTP Cyclohydrotase & DHBP Synthase	0419 (CT270)	pbp3	Transglycolase/Transpeptidase
0532 (CT405)	ribC	Riboflavin Synthase	0421 (CT272)	yabC	PBP2B Family Methyltransferase
			Cellular Processes		
			Cell Division		
			0959 (CT808)	cafE	Axial Filament Protein
			0880 (CT739)	ftsK	Cell Division Protein FtsK

0903 (CT760)	ftsW	Cell Division Protein FtsW
0972 (CT820)	ftsY	Cell Division Protein FtsY
0617 (CT498)	gidA	FAD-dependent Oxidoreductase
0805 (CT582)	minD	Chromosome Partitioning ATPase
0850 (CT709)	mreB	Rod Shape Protein-Sugar Kinase
0867 (CT726)	rodA	Rod Shape Protein
0684 (CT688)	parB	Chromosome Partitioning Protein

Detoxification

0057 (CT294)	sodM	Superoxide Dismutase (Mn)
0778 (CT603)	ahpC	Thio-specific Antioxidant (TSA) Peroxidase

Signal Transduction

0148 (CT145)		S/T Protein Kinase
0584 (CT467)	atoS	Two-Component Sensor
0294 (CT235)		cAMP-Dependent Protein Kinase Regulatory Subunit
0712 (CT664)		(FHA domain)
0478 (CT379)	hflX	GTP Binding Protein
0703 (CT673)		S/T Protein Kinase
0095 (CT301)		S/T Protein Kinase
0397 (CT259)		PP2C Phosphatase Family
0037 (CT337)	ptsH	PTS Phosphocarrier Protein Hpr
0038 (CT336)	ptsI	PTS PEP Phosphotransferase
0060 (CT291)	ptsN_1	PTS IIA Protein_1
0061 (CT290)	ptsN_2	PTS IIA Protein + HTH DNA-Binding Domain
0262 (CT218)	surE	SurE-like Acid Phosphatase
0838 (CT698)	thdF	Thiophene/Furan Oxidation Protein
0693 (CT683)	TPR	Repeats-CT683 Hypothetical Protein
0321 (CT092)	ychF	GTP Binding Protein
0544 (CT418)	yhbZ	GTP binding protein
0844 (CT703)	yphC	GTPase/GTP-binding protein

Standard Protein Secretion

0115 (CT025)	ffh	Signal Recognition Particle GTPase
0363 (CT060)	flhA	Flagellar Secretion Protein
0858 (CT717)	flil	Flagellum-specific ATP Synthase
0704 (CT672)	flin	Flagellar Motor Switch Domain/YscQ family
0815 (CT572)	gspD	Gen. Secretion Protein D
0816 (CT571)	gspE	Gen. Secretion Protein E
0817 (CT570)	gspF	Gen. Secretion Protein F
0359 (CT064)	lepA	GTPase
0110 (CT020)	lepB	Signal Peptidase I
0535 (CT408)	lspA	Lipoprotein Signal Peptidase
0260 (CT141)	secA_1	Protein Translocase Subunit_1
0841 (CT701)	secA_2	Translocase SecA_2
0564 (CT448)	secDsecE	Protein Export Proteins SecD/SecE (fusion)
0075 (CT321)	secE	Preprotein Translocase
0629 (CT510)	secY	Translocase
0848 (CT707)	tig	Trigger Factor-Peptidyl-prolyl Isomerase

Transport-Related Proteins

0486		Hypothetical Proline Permease
0289 (CT230)	aaaT	Neutral Amino Acid (Glutamate) Transporter
0691 (CT685)	abcX	ABC Transporter ATPase
1031 (CT374)	arcD	Arginine/Ornithine Antiporter
0482 (CT381)	artJ	Arginine Periplasmic Binding Protein
0836 (CT554)	brnQ	Amino Acid (Branched) Transport
0536 (CT409)	dagA_1	D-Ala/Gly Permease_1
0876 (CT735)	dagA_2	D-Alanine/Glycine Permease_2
0682 (CT690)	dppD	ABC ATPase Dipeptide Transport
0683 (CT689)	dppF	ABC ATPase Dipeptide Transport
0280 (CT689)	dppF	Dipeptide Transporter ATPase
0785 (CT596)	exbB	Macromolecule Transporter
0784 (CT597)	exbD	Biopolymer Transport Protein
0604 (CT486)	fliY	Glutamine Binding Protein
0192 (CT129)	glnP	ABC Amino Acid Transporter Permease
0191 (CT130)	glnQ	ABC Amino Acid Transporter ATPase
0528 (CT401)	gltT	Glutamate Symport
0286 (CT194)	mgTE	Mg ²⁺ Transporter (CBS Domain)
0413 (CT264)	msbA	Transport ATP Binding Protein
0290 (CT231)		Na ⁺ -dependent Transporter
0195 (CT198)	oppA_1	Oligopeptide Binding Protein_1
0196 (CT198)	oppA_2	Oligopeptide Binding Protein_2
0197 (CT139)	oppA_3	Oligopeptide Binding Protein_3
0198 (CT175)	oppA_4	Oligopeptide Binding Protein_4
0599 (CT480)	oppA_5	Oligopeptide Binding Lipoprotein_5
0199 (CT199)	oppB_1	Oligopeptide Permease_1
0598 (CT479)	oppB_2	Oligopeptide Permease_2
0200 (CT200)	oppC_1	Oligopeptide Permease_1
0597 (CT478)	oppC_2	Oligopeptide Permease_2
0201 (CT201)	oppD	Oligopeptide Transport ATPase

0202 (CT202)	oppF	Oligopeptide Transport ATPase
0231 (CT180)	tauB	ABC Transport ATPase (Nitrate/Fe)
0782 (CT599)	tolB	Macromolecule Transporter
0969 (CT817)	tyrP_1	Tyrosine Transport_1
0970 (CT818)	tyrP_2	Tyrosine Transport_2
0665 (CT544)	uhpC	Hexosphosphate Transport
0282 (CT216)	xasA	Amino Acid Transporter
0207 (CT204)	ybhI	dicarboxylate Translocator
0971 (CT819)	yccA	Transport Permease
0248 (CT152)	ycfV	ABC Transporter ATPase
1014 (CT856)	ychM	Sulfate Transporter
0736 (CT641)	ygeD	Efflux Protein
0680 (CT692)	ygo4	Phosphate Permease
0723 (CT653)	yhbG	ABC Transporter ATPase
0023 (CT348)	yjiK	ABC Transporter Protein ATPase
0127 (CT034)	ytfF	Cationic Amino Acid Transporter
0349 (CT067)	ytgA	Solute Protein Binding Family
0348 (CT068)	ytgB	ABC transporter ATPase
0347 (CT069)	ytgC	Integral Membrane Protein
0346 (CT070)	ytgD	Integral Membrane Protein
1012 (CT854)	zseB	ABC Transporter Permease
0868 (CT727)	zntA	Metal Transport P-type ATPase
0279		Possible ABC Transporter Permease Protein (Metal Transport Protein)
0543 (CT417)		ABC Transporter
0692 (CT684)		ABC Transporter
0542 (CT416)		ABC Transporter ATPase
0690 (CT686)		ABC Transporter Membrane Protein
0541 (CT415)		solute binding protein

Type-III Secretion

0323 (CT090)	lcrD	Low Calcium Response D
0324 (CT089)	lcrE	Low Calcium Response E
0811 (CT576)	lcrH_1	Low Ca Response Protein H_1
1021 (CT862)	lcrH_2	Low Calcium Response_2
0325 (CT088)	sydE	Secretion Chaperone
0702 (CT674)	yscC	Yop C/Gen Secretion Protein D
0828 (CT559)	yscJ	Yop Translocation J
0826 (CT561)	yscL	Yop Translocation L
0707 (CT669)	yscN	Yop N (Flagellar-Type ATPase)
0825 (CT562)	yscR	Yop Translocation R
0824 (CT563)	yscS	YopS Translocation Protein
0823 (CT564)	yscT	YopT Translocation T
0322 (CT091)	yscU	Yop Translocation Protein U

Central Intermediary Metabolism**Glycogen Metabolism**

0856 (CT715)		UDP-Glucose Pyrophosphorylase
0948 (CT798)	glgA	Glycogen Synthase
0475 (CT866)	glgB	Glucan Branching Enzyme
0607 (CT489)	glgC	Glucose-1-P Adenyltransferase
0307 (CT248)	glgP	Glycogen Phosphorylase
0388 (CT042)	glgX	Glycogen Hydrolase (debranching)
0326 (CT087)	malQ	Glucanotransferase
0851 (CT710)	pckA	Phosphoenolpyruvate Carboxykinase

Phosphorous & Sulfur

0548 (CT435)	cysJ	Sulfite Reductase
0920 (CT774)	cysQ	Sulfite Synthesis/Biphosphate Phosphatase
0025 (CT346)	atsA	Sulphohydrolase
0918 (CT772)	ppa	Inorganic Pyrophosphatase

DNA Replication, Modification, Repair & Recombination**DNA Mismatch Repair**

0505		3-Methyladenine DNA Glycosylase
0812 (CT575)	mutL	DNA Mismatch Repair
0941 (CT792)	mutS	DNA Mismatch Repair
0402 (CT107)	mutY	Adenine Glycosylase
0732 (CT625)	nfo	Endonuclease IV
0837 (CT697)	nth	Endonuclease III

DNA Modification

0596 (CT477)	ada	Methyltransferase
0114 (CT024)	hemK	A/G-specific Methylase
0891 (CT748)	mfd	Transcription-Repair Coupling
0620 (CT501)	ruvA	Holliday Junction Helicase
0390 (CT040)	ruvB	Holliday Junction Helicase
0621 (CT502)	ruvC	Crossover Junction Endonuclease
0053 (CT298)	sms	Sms Protein
0773 (CT607)	ung	Uracil DNA Glycosylase
1062 (CT329)	xseA	Exodexyribonuclease VII

DNA Recombination

0762 (CT650) recA RecA Recombination Protein
 0738 (CT639) recB Exodeoxyribonuclease V, Beta
 0737 (CT640) recC Exodeoxyribonuclease V, Gamma
 0123 (CT033) recD_1 Exodeoxyribonuclease V (Alpha Subunit)_1
 0752 (CT652) recD_2 Exodeoxyribonuclease V, Alpha_2
 0339 (CT074) recF ABC Superfamily ATPase
 0340 (CT074) (frame-shift with 0339)
 0563 (CT447) recJ ssDNA Exonuclease
 0299 (CT240) recR Recombination Protein

DNA Replication

0309 (CT250) dnaA_1 Replication Initiation Protein_1
 0424 (CT275) dnaA_2 Replication Initiation Factor_2
 0616 (CT497) dnaB Replicative DNA Helicase
 0666 (CT545) dnaE DNA Pol III Alpha
 0942 (CT794) dnaG DNA Primase
 0338 (CT075) dnaN DNA Pol III (Beta)
 0410 (CT261) dnaQ_1 DNA Pol III Epsilon Chain_1
 0655 (CT536) dnaQ_2 DNA Pol III Epsilon Chain_2
 0040 (CT334) dnaX_1 DNA Pol III Gamma and Tau_1
 0272 (CT187) dnaX_2 DNA Pol III Gamma and Tau_2
 0149 (CT146) dnlJ DNA Ligase
 0274 (CT189) gyrA_1 DNA Gyrase Subunit A_1
 0716 (CT660) gyrA_2 DNA Gyrase Subunit A_2
 0275 (CT190) gyrB_1 DNA Gyrase Subunit B_1
 0715 (CT661) gyrB_2 DNA Gyrase Subunit B_2
 0416 (CT267) himD Integration Host Factor Alpha
 0612 (CT493) polA DNA Polymerase I
 0924 (CT778) priA Primosomal Protein N'
 0386 (CT044) ssb SS DNA Binding Protein
 0835 (CT555) SWI/SNF family helicase_1
 0849 (CT708) SWI/SNF family helicase_2
 0769 (CT643) topA DNA Topoisomerase I-Fused to SWI Domain
 0024 (CT347) xerC Integrase/recombinase
 1024 (CT864) xerD Integrase/recombinase

Eukaryotic-Type Chromatin Factors

0886 (CT743) hctA Histone-Like Developmental Protein
 0384 (CT046) hctB Histone-like Protein 2
 0878 (CT737) SET Domain protein
 0577 (CT460) SWIB (YM74) Complex Protein

UVR Exinuclease Repair System

0096 (CT333) uvrA Exinuclease ABC Subunit A
 0801 (CT586) uvrB Exinuclease ABC Subunit B
 0940 (CT791) uvrC Exinuclease ABC, Subunit C
 0772 (CT608) uvrD DNA Helicase

Energy Metabolism

Aerobic

0855 (CT714) gpdA Glycerol-3-P Dehydrogenase
 0743 (CT634) nqrA Ubiquinone Oxidoreductase, Alpha
 0427 (CT278) nqr2 NADH (Ubiquinone) Dehydrogenase
 0428 (CT279) nqr3 NADH (Ubiquinone) Oxidoreductase, Gamma
 0429 (CT280) nqr4 NADH (Ubiquinone) Reductase 4
 0430 (CT281) nqr5 NADH (Ubiquinone) Reductase 5
 0883 (CT740) nqr6 Phenolhydrolase/NADH (Ubiquinone) Oxidoreductase 6

ATP Biogenesis and metabolism

0351 (CT065) adt_1 ADP/ATP Translocase_1
 0614 (CT495) adt_2 ADP/ATP Translocase_2
 0088 (CT308) atpA ATP Synthase Subunit A
 0089 (CT307) atpB ATP Synthase Subunit B
 0090 (CT306) atpD ATP Synthase Subunit D
 0086 (CT310) atpE ATP Synthase Subunit E
 0091 (CT305) atpI ATP Synthase Subunit I
 0092 (CT304) atpK ATP Synthase Subunit K
 0860 (CT719) flIF Flagellar M-Ring Protein

Electron Transport Chain

0102 (CT013) cydA Cytochrome Oxidase Subunit I
 0103 (CT014) cydB Cytochrome Oxidase Subunit II
 0364 (CT059) ferredoxin
 0084 (CT312) Predicted Ferredoxin

Glycolysis & Gluconeogenesis

0281 (CT215) dhna Predicted 1,6-Fructose Biphosphate Aldolase
 0800 (CT587) eno Enolase
 0624 (CT505) gapA Glyceraldehyde-3-P Dehydrogenase
 0056 (CT295) mrsA Phosphomannomutase
 0967 (CT815) pgm Phosphoglucomutase

0160 (CT207) pfkA_1 Fructose-6-P Phosphotransferase_1
 0208 (CT205) pfkA_2 Fructose-6-P Phosphotransferase_2
 1025 (CT378) pgi Glucose-6-P Isomerase
 0679 (CT693) pgk Phosphoglycerate Kinase
 0863 (CT722) pgmA Phosphoglycerate Mutase
 0097 (CT332) pyk Pyruvate Kinase
 1063 (CT328) tpiS Triosephosphate Isomerase

Pentose Phosphate Pathway

0239 (CT186) devB Glucose-6-P Dehydrogenase (DevB family)
 1060 (CT331) dxs Transketolase
 0360 (CT063) gnd 6-Phosphogluconate Dehydrogenase
 0185 (CT121) rpe Ribulose-P Epimerase
 0141 (CT213) rpiA Ribose-5-P Isomerase A
 0083 (CT313) tal Transaldolase
 0893 (CT750) tktB Transketolase
 0238 (CT185) zwf Glucose-6-P Dehydrogenase

Pyruvate Dehydrogenase

0833 (CT557) lpdA Lipoamide Dehydrogenase
 0436 (CT285) lplA_1 Lipoate Protein Ligase-Like Protein
 0618 (CT499) lplA_2 Lipoate-Protein Ligase A
 0033 (CT340) pdhA&BOxoisovalerate Dehydrogenase α/β Fusion
 0304 (CT245) pdhA Pyruvate Dehydrogenase Alpha
 0305 (CT246) pdhB Pyruvate Dehydrogenase Beta
 0306 (CT247) pdhC Dihydrolipoamide Acetyltransferase

TCA Cycle

0495 (CT390) aspC Aspartate Aminotransferase
 1013 (CT855) fumC Fumarate Hydratase
 1028 (CT376) mdhC Malate Dehydrogenase
 0789 (CT592) sdhA Succinate Dehydrogenase
 0790 (CT591) sdhB Succinate Dehydrogenase
 0788 (CT593) sdhC Succinate Dehydrogenase
 0378 (CT054) sucA Oxoglutarate Dehydrogenase
 0377 (CT055) sucB_1 Dihydrolipoamide Succinyltransferase_1
 0527 (CT400) sucB_2 Dihydrolipoamide Succinyltransferase_2
 0973 (CT821) sucC Succinyl-CoA Synthetase, Beta
 0974 (CT822) sucD Succinyl-CoA Synthetase, Alpha

Protein Folding, Assembly & Modification

Chaperones

0949 (CT799) ctc General Stress Protein
 0534 (CT407) dksA DnaK Suppressor
 0032 (CT341) dnaJ Heat Shock Protein J
 0503 (CT396) dnaK Hsp-70
 0134 (CT110) groEL_1 Hsp-60_1
 0777 (CT604) groEL_2 Hsp-60_2
 0898 (CT755) groEL_3 Hsp-60_3
 0135 (CT111) groES 10KDa Chaperonin
 0502 (CT395) grpE HSP-70 Cofactor
 0661 (CT541) mip FKBP-type Peptidyl-prolyl Cis-Trans Isomerase

Proteases

0144 (CT113) clpB Clp Protease ATPase
 0437 (CT286) clpC ClpC Protease
 0520 (CT431) clpP_1 CLP Protease
 0847 (CT706) clpP_2 CLP Protease Subunit
 0846 (CT705) clpX CLP Protease ATPase
 0269 (CT138) Dipeptidase
 0998 (CT841) ftsH ATP-dependent Zinc Protease
 0030 (CT343) gcp_1 O-Sialoglycoprotein Endopeptidase_1
 0194 (CT197) gcp_2 O-Sialoglycoprotein Endopeptidase_2
 0979 (CT823) htrA DO Serine Protease
 0957 (CT806) ide Insulinase family/Protease III
 0027 (CT344) lon Lon ATP-dependent Protease
 1017 (CT859) lytB Metalloprotease
 1009 (CT851) map Methionine Aminopeptidase
 0385 (CT045) pepA Leucyl Aminopeptidase A
 0136 (CT112) pepF Oligopeptidase
 0813 (CT574) pepP Aminopeptidase P
 0613 (CT494) sohB Protease
 0555 (CT441) tsp Tail-Specific Protease
 0344 (CT072) yaeL Metalloprotease
 0981 (CT824) Zinc Metalloprotease (insulinase family)

Protein Isomerases

0227 (CT176) dsbB Disulfide bond Oxidoreductase
 0786 (CT595) dsbD Thio-disulfide Interchange Protein
 0228 (CT177) dsbG Disulfide Bond Chaperone
 0933 (CT783) Predicted Disulfide Bond Isomerase
 0926 (CT780) Thioredoxin Disulfide Isomerase

Transcription**RNA Degradation**

0999	(CT842)	pnp	Polyribonucleotide Nucleotidyltransferase
0054	(CT297)	rnc	Ribonuclease III
0119	(CT029)	rnhB_1	Ribonuclease HII_1
1068	(CT008)	rnhB_2	Ribonuclease HII_2
0934	(CT784)	rnpA	Ribonuclease P Protein Component
0504	(CT397)	vacB	Ribonuclease Family

RNA Elongation & Termination Factors

0741	(CT636)	greA	Transcription Elongation Factor
0316	(CT097)	nusA	N Utilization Protein A
0076	(CT320)	nusG	Transcriptional Antitermination
0845	(CT704)	pcnB_1	Poly A Polymerase_1
0966	(CT410)	pcnB_2	PolyA Polymerase_2
0610	(CT491)	rho	Transcription Termination Factor

RNA Methylases

0674	(CT553)	fmu	RNA Methyltransferase
1059	(CT354)	kgsA	Dimethyladenosine Transferase
0187	(CT133)		Predicted Methylase
0530	(CT403)	spoU_1	rRNA Methylase_1
0660	(CT540)	spoU_2	rRNA Methylase_2
0117	(CT027)	trmD	tRNA (Guanine N-1)-Methyltransferase
0885	(CT742)	ycgA	rRNA Methyltransferase
0986	(CT829)	yggH	Predicted rRNA Methylase
0987	(CT830)	ytgB	Predicted rRNA Methylase

RNA Modification

0649	(CT530)	fmt	Methionyl tRNA Formyltransferase
0910	(CT766)	miaA	tRNA Pyrophosphate Transferase
0719	(CT658)	sfbB	Predicted Pseudouridine Synthase
0219	(CT193)	tgt	Queuine tRNA Ribosyl Transferase
0580	(CT463)	truA	Pseudouridylylase Synthase I
0319	(CT094)	truB	tRNA Pseudouridine Synthase
0403	(CT106)	ycgC	Predicted Pseudouridine Synthetase Family
0864	(CT723)	yjbC	Predicted Pseudouridine Synthase

RNA Polymerase & Transcription Regulators

0586	(CT468)	atoC	Two-Component Regulator
0362	(CT061)	rpsD	Sigma-28/WhiG Family
0501	(CT394)	hrcA	HTH Transcriptional Repressor
0793	(CT588)	rbsU	Sigma Regulatory Family Protein—PP2C Phosphatase (RsbW Antagonist)
0626	(CT507)	rpoA	RNA Polymerase Alpha
0081	(CT315)	rpoB	RNA Polymerase Beta
0082	(CT314)	rpoC	RNA Polymerase Beta'
0756	(CT615)	rpoD	RNA Polymerase Sigma-66
0771	(CT609)	rpoN	RNA Polymerase Sigma-54
0511	(CT424)	rsbV_1	Sigma Regulatory Factor_1
0909	(CT765)	rsbV_2	Sigma Factor Regulator_2
0670	(CT549)	rsbW	Sigma Regulatory Factor-Histidine Kinase
0750	(CT630)	tctD	HTH Transcriptional Regulatory Protein + Receiver Domain
1069	(CT009)	yfgA	HTH Transcriptional Regulator

Translation**Amino Acyl tRNA Synthetase**

0892	(CT749)	alaS	Alanyl tRNA Synthetase
0570	(CT454)	argS	Arginyl tRNA Synthetase
0662	(CT542)	aspS	Aspartyl tRNA Synthetase
0932	(CT782)	cysS	Cysteinyl tRNA Synthetase
0003	(CT003)	gatA	Glu tRNA Gln Amidotransferase (A subunit)
0004	(CT004)	gatB	Glu tRNA Gln Amidotransferase (B Subunit)
0002	(CT002)	gatC	Glu tRNA Gln Amidotransferase (C subunit)
0560	(CT445)	glxX	Glutamyl-tRNA Synthetase
0946	(CT796)	glyQ	Glycyl tRNA Synthetase
0663	(CT543)	hisS	Histidyl tRNA Synthetase
0109	(CT019)	ileS	Isoleucyl-tRNA Synthetase
0153	(CT209)	leuS	Leucyl tRNA Synthetase
0931	(CT781)	lysS	Lysyl tRNA Synthetase
0122	(CT032)	metG	Methionyl-tRNA Synthetase
0993	(CT836)	pheS	Phenylalanyl tRNA Synthetase, Alpha
0594	(CT475)	pheT	Phenylalanyl tRNA Synthetase Beta
0500	(CT393)	proS	Prolyl tRNA Synthetase
0870	(CT729)	serS	Seryl tRNA Synthetase_2
0806	(CT581)	thrS	Threonyl tRNA Synthetase
0802	(CT585)	trpS	Tryptophanyl tRNA Synthetase
0361	(CT062)	tyrS	Tyrosyl tRNA Synthetase
0094	(CT302)	valS	Valyl tRNA Synthetase

Peptide Chain Initiation, Elongation & Termination

1067	(CT353)	def	Polypeptide Deformylase
0184	(CT122)	efp_1	Elongation Factor P_1
0895	(CT752)	efp_2	Elongation Factor P_2
0550	(CT437)	fusA	Elongation Factor G
0073	(CT323)	infA	Initiation Factor IF-1
0317	(CT096)	infB	Initiation Factor-2
0990	(CT833)	infC	Initiation Factor 3
0113	(CT023)	pfrA	Peptide Chain Releasing Factor 1
0576	(CT459)	prfB	Peptide Chain Release Factor 2
0950	(CT800)	pth	Peptidyl tRNA Hydrolase
0318	(CT095)	rbfA	Ribosome Binding Factor A
0699	(CT677)	rrf	Ribosome Releasing Factor
0697	(CT679)	tsf	Elongation Factor TS
0074	(CT322)	tufA	Elongation Factor Tu

Ribosomal Proteins

0078	(CT318)	r11	L1 Ribosomal Protein
0644	(CT525)	r12	L2 Ribosomal Protein
0647	(CT528)	r13	L3 Ribosomal Protein
0646	(CT527)	r14	L4 Ribosomal Protein
0635	(CT516)	r15	L5 Ribosomal Protein
0633	(CT514)	r16	L6 Ribosomal Protein
0080	(CT316)	r17	L7/L12 Ribosomal Protein
0953	(CT803)	r19	L9 Ribosomal Protein
0079	(CT317)	r110	L10 Ribosomal Protein
0077	(CT319)	r111	L11 Ribosomal Protein
0247	(CT125)	r113	L13 Ribosomal Protein
0637	(CT518)	r114	L14 Ribosomal Protein
0630	(CT511)	r115	L15 Ribosomal Protein
0640	(CT521)	r116	L16 Ribosomal Protein
0625	(CT506)	r117	L17 Ribosomal Protein
0632	(CT513)	r118	L18 Ribosomal Protein
0118	(CT028)	r119	L19 Ribosomal Protein
0992	(CT835)	r120	L20 Ribosomal Protein
0546	(CT420)	r121	L21 Ribosomal Protein
0642	(CT523)	r122	L22 Ribosomal Protein
0645	(CT526)	r123	L23 Ribosomal Protein
0636	(CT517)	r124	L24 Ribosomal Protein
0545	(CT419)	r127	L27 ribosomal protein
0327	(CT086)	r128	L28 Ribosomal Protein
0639	(CT520)	r129	L29 Ribosomal Protein
0112	(CT022)	r131	L31 Ribosomal Protein
0961	(CT810)	r132	L32 Ribosomal Protein
0250	(CT150)	r133	L33 Ribosomal Protein
0935	(CT785)	r134	L34 Ribosomal Protein
0991	(CT834)	r135	L35 Ribosomal Protein
0936	(CT786)	r136	L36 Ribosomal Protein
0315	(CT098)	rs1	S1 Ribosomal Protein
0696	(CT680)	rs2	S2 Ribosomal Protein
0641	(CT522)	rs3	S3 Ribosomal Protein
0733	(CT626)	rs4	S4 Ribosomal Protein
0631	(CT512)	rs5	S5 Ribosomal Protein
0951	(CT801)	rs6	S6 Ribosomal Protein
0551	(CT438)	rs7	S7 Ribosomal Protein
0634	(CT515)	rs8	S8 Ribosomal Protein
0246	(CT126)	rs9	S9 Ribosomal Protein
0549	(CT436)	rs10	S10 Ribosomal Protein
0627	(CT508)	rs11	S11 Ribosomal Protein
0552	(CT439)	rs12	S12 Ribosomal Protein
0628	(CT509)	rs13	S13 Ribosomal Protein
0937	(CT787)	rs14	S14 Ribosomal Protein
1000	(CT843)	rs15	S15 Ribosomal Protein
0116	(CT026)	rs16	S16 Ribosomal Protein
0638	(CT519)	rs17	S17 Ribosomal Protein
0952	(CT802)	rs18	S18 Ribosomal Protein
0643	(CT524)	rs19	S19 Ribosomal Protein
0754	(CT617)	rs20	S20 Ribosomal Protein
0031	(CT342)	rs21	S21 Ribosomal Protein

Other Categories**Chlamydia-Specific Proteins**

0561	(CT446)	Euo	CHLPS Euo Protein
0804	(CT583)	Gp6D	CHLTR Plasmid Paralog
0186	(CT119)		Similarity to IncA_1
0291	(CT232)	incB	Inclusion Membrane Protein B
0292	(CT233)	incC	Inclusion Membrane Protein C
1026	(CT377)		LtuA Protein
0333	(CT080)		LtuB Protein
0005	(CT871)	pmp_1	Polymorphic Outer Membrane Protein G Family

0013 (CT871)	pmp_2	Polymorphic Outer Membrane Protein G Family	0734 (CT627)	yceA	YceA Hypothetical Protein
0014 (CT871)	pmp_3	Polymorphic Outer Membrane Protein G Family	0954 (CT804)	ychB	Predicted Kinase
0015 (CT871)	pmp_3	PMP_3 (frame-shift with 0014)	0261 (CT217)	ydaO	PP-Loop Superfamily ATPase
0016 (CT874)	pmp_4	Polymorphic Outer Membrane Protein G Family	0245 (CT127)	ydhO	Polysaccharide Hydrolase-Invasin Repeat Family
0017 (CT871)	pmp_4	PMP_4 (frame-shift with 0016)	0573 (CT457)	yebC	YebC Family Hypothetical Protein
0018 (CT874)	pmp_5	Polymorphic Outer Membrane Protein G Family	0689 (CT687)	yfhO_1	NifS-related Aminotransferase_1
0019 (CT871)	pmp_5	PMP_5 (frame-shift with 0018)	0862 (CT721)	yfhO_2	NifS-related Aminotransferase_2
0444 (CT871)	pmp_6	Polymorphic Outer Membrane Protein G/I Family	0547 (CT434)	ygbB	YgbB Family Hypothetical Protein
0445 (CT871)	pmp_7	Polymorphic Outer Membrane Protein G Family	0237 (CT184)	yggF	YggF Family Hypothetical Protein
0446 (CT871)	pmp_8	Polymorphic Outer Membrane Protein G Family	0775 (CT606)	yggV	YggV Family Hypothetical Protein
0447 (CT871)	pmp_9	Polymorphic Outer Membrane Protein G/I Family	0396 (CT258)	yhfO_3	NifS-related Aminotransferase_3
0450 (CT871)	pmp_10	Polymorphic Outer Membrane Protein G Family	0605 (CT487)	yhhF	Predicted Methylase
0449 (CT871)	pmp_10	PMP_10 (Frame-shift with 0450)	0575 (CT458)	yhhY	Amino Group Acetyl Transferase
0451 (CT871)	pmp_11	Polymorphic Outer Membrane Protein G Family	0592 (CT473)	yldD	YidD Family
0452 (CT874)	pmp_12	Polymorphic Outer Membrane Protein (truncated) A/I Family	0982 (CT825)	yigN	YigN Family Hypothetical Protein
0453 (CT871)	pmp_13	Polymorphic Outer Membrane Protein G Family	0657 (CT537)	yjeE	YjeE Hypothetical Protein
0454 (CT872)	pmp_14	Polymorphic Outer Membrane Protein H Family	0768 (CT644)	yohI	YohI Predicted Oxidoreductase
0466 (CT869)	pmp_15	Polymorphic Outer Membrane Protein E Family	0336 (CT077)	yoiL	YoiL Hypothetical Protein
0467 (CT869)	pmp_16	Polymorphic Outer Membrane Protein E Family	0217 (CT140)	ypdP	YpdP Hypothetical Protein
0468 (CT869)	pmp_17	Polymorphic Outer Membrane Protein E Family	0140 (CT212)	yqde	YqdE Hypothetical Protein
0469 (CT869)	pmp_17	PMP_17 (Frame-shift with 0468)	0263 (CT221)	yqfU	YqfU Hypothetical Protein
0470 (CT869)	pmp_17	PMP_17 (Frame-shift with 0469)	0139 (CT211)	yqgE	YqgE Hypothetical Protein
0471 (CT870)	pmp_18	Polymorphic Outer Membrane Protein E/F Family	0270 (CT137)	ywlC	SuA5 Superfamily-related Protein
0539 (CT412)	pmp_19	Polymorphic Membrane Protein A Family	0879 (CT738)	yyeC	Metal Dependent Hydrolase
0540 (CT413)	pmp_20	Polymorphic Membrane Protein B Family			
0963 (CT812)	pmp_21	Polymorphic Membrane Protein D Family			
0562		CHLPS 43 kDa Protein Homolog_1	0001 (CT001)	CT001	Hypothetical Protein
0927		CHLPS 43 kDa Protein Homolog_2	0020 (CT351)	CT351	Hypothetical Protein
0928		CHLPS 43 kDa Protein Homolog_3	0021 (CT350)	CT350	Hypothetical Protein
0929		CHLPS 43 kDa Protein Homolog_4	0026 (CT345)	CT345	Hypothetical Protein
0728 (CT622)		CHLPN 76kDa Homolog_1 (CT622)	0035 (CT339)	CT339	Hypothetical Protein
0729 (CT623)		CHLPN 76kDa Homolog_2 (CT623)	0036 (CT338)	CT338	Hypothetical Protein
0133 (CT109)		CHLPS Hypothetical Protein	0055 (CT296)	CT296	Hypothetical Protein
0332 (CT081)		CHLTR T2 Protein	0062 (CT289)	CT289	Hypothetical Protein
			0065 (CT288)	CT288	Hypothetical Protein
			0068 (CT360)	CT360	Hypothetical Protein
			0071 (CT325)	CT325	Hypothetical Protein
			0072 (CT324)	CT324	Hypothetical Protein
			0085 (CT311)	CT311	Hypothetical Protein
			0087 (CT309)	CT309	Hypothetical Protein
			0093 (CT303)	CT303	Hypothetical Protein
			0100 (CT011)	CT011	Hypothetical Protein
			0104 (CT017)	CT017	Hypothetical Protein
			0105 (CT016)	CT016	Hypothetical Protein
			0107 (CT058)	CT058	Hypothetical Protein_1
			0108 (CT018)	CT018	Similarity
			0111 (CT021)	CT021	Hypothetical Protein
			0121 (CT031)	CT031	Hypothetical Protein
			0129 (CT036)	CT036	Similarity
			0145 (CT114)	CT114	Hypothetical Protein
			0150 (CT147)	CT147	Hypothetical Protein
			0152 (CT149)	CT149	Hypothetical Protein
			0176 (CT153)	CT153	Hypothetical Protein
			0188 (CT132)	CT132	Hypothetical Protein
			0189 (CT131)	CT131	Hypothetical Protein
			0206 (CT203)	CT203	Hypothetical Protein
			0229 (CT178)	CT178	Hypothetical Protein
			0230 (CT179)	CT179	Hypothetical Protein
			0234 (CT181)	CT181	Hypothetical Protein
			0249 (CT151)	CT151	Hypothetical Protein
			0253 (CT144)	CT144	Hypothetical Protein_1
			0254 (CT143)	CT143	Hypothetical Protein_1
			0255 (CT142)	CT142	Hypothetical Protein_1
			0256 (CT144)	CT144	Hypothetical Protein_2
			0257 (CT143)	CT143	Hypothetical Protein_2
			0259 (CT142)	CT142	Hypothetical Protein_2
			0276 (CT191)	CT191	Hypothetical Protein
			0288 (CT195)	CT195	Hypothetical Protein
			0293 (CT234)	CT234	Hypothetical Protein
			0301 (CT242)	CT368	Hypothetical Protein
			0303 (CT244)	CT244	Hypothetical Protein
			0308 (CT249)	CT249	Similarity
			0312 (CT101)	CT101	Hypothetical Protein
			0328 (CT085)	CT085	Hypothetical Protein
			0330 (CT083)	CT083	Hypothetical Protein
			0331 (CT082)	CT082	Hypothetical Protein
			0334 (CT079)	CT079	Similarity
			0342 (CT073)	CT073	Hypothetical Protein
			0343 (CT073)	(frame-shift with 0342)	
			0350 (CT066)	CT066	Hypothetical Protein
			0369 (CT058)	CT058	Hypothetical Protein_2



Homologs to CHLTR Hypothetical Coding Genes

Miscellaneous Enzymes/Conserved Proteins

0193	argR	Possible Arginine Repressor
1046		Aromatic Amino Acid Hydroxylase
0232		Similarity to 5'-Methylthioadenosine Nucleosidase
0128 (CT035)		Biotin Protein Ligase
0513 (CT426)		Fe-S Oxidoreductase_1
0911 (CT767)		Fe-S Oxidoreductase_2
0373 (CT057)	gcpE	GcpE Protein
0407 (CT103)		HAD Superfamily Hydrolase/Phosphatase
0917 (CT771)		Hydrolase/Phosphatase Homolog
0488 (CT385)	ycfF	HIT Family Hydrolase
0701 (CT675)	karG	Arginine Kinase
0526 (CT399)	kpsF	GutQ/KpsF Family Sugar-P Isomerase
0919 (CT773)	ldh	Leucine Dehydrogenase
0022 (CT349)	maf	Maf protein
0997 (CT840)	mesJ	PP-loop superfamily ATPase
0151 (CT148)	mhpA	Monooxygenase
0730 (CT624)	mvnI	Integral Membrane Protein
0861 (CT720)		NifU-Related Protein
0479 (CT380)	phnP	Metal Dependent Hydrolase
0106 (CT015)	phoH	ATPase
0329 (CT084)		Phospholipase D Superfamily
0435 (CT284)		Phospholipase D Superfamily
0581 (CT464)		Phosphoglycolate Phosphatase
0897 (CT754)		Predicted Phosphohydrolase
0509 (CT422)		Predicted Metalloenzyme
1030 (CT375)		Predicted D-Amino Acid Dehydrogenase
0531 (CT404)		SAM Dependent Methyltransferase
0337 (CT076)	smpB	Small Protein B
0394 (CT256)	tlyC_1	CBS Domain Protein (Hemolysin Homolog)_1
0510 (CT423)	tlyC_2	CBS Domains (Hemolysin Homolog)_2
0382 (CT048)	yabC	SAM-Dependent Methyltransferase
0787 (CT594)	yabD	PHP Superfamily (Urease/Pyrimidinase) Hydrolase
0611 (CT492)	yacE	Predicted Phosphatase/Kinase
0579 (CT462)	yacM	Sugar Nucleotide Phosphorylase
0578 (CT461)	yael	Phosphohydrolase
0345 (CT071)	yaeM	CT071 Hypothetical Protein
0566 (CT450)	yaeS	YaeS family Hypothetical Protein
0591 (CT472)	yagE	YagE family
0039 (CT335)	ybaB	YbaB family Hypothetical Protein
0101 (CT012)	ybbP	YbbP family Hypothetical Protein
0915 (CT769)	ybeB	iojap Superfamily Ortholog
0137 (CT108)	ybgI	ACR family
0529 (CT402)	ycaH	ATPase
0438 (CT287)	ycbF	PP-loop Superfamily ATPase

0370	(CT058)	CT058 Hypothetical Protein_3	0708	(CT668)	CT668 Hypothetical Protein
0374	(CT056)	CT056 Hypothetical Protein	0709	(CT667)	CT667 Hypothetical Protein
0379	(CT053)	CT053 Hypothetical Protein	0710	(CT666)	CT666 Hypothetical Protein
0381	(CT326)	CT326 Similarity	0711	(CT665)	CT665 Hypothetical Protein
0383	(CT047)	CT047 Hypothetical Protein	0713	(CT663)	CT663 Hypothetical Protein
0387	(CT043)	CT043 Hypothetical Protein	0717	(CT656)	CT656 Hypothetical Protein
0389	(CT041)	CT041 Hypothetical Protein	0718	(CT657)	CT657 Hypothetical Protein
0393	(CT038)	CT038 Hypothetical Protein	0720	(CT659)	CT659 Hypothetical Protein
0395	(CT257)	CT257 Hypothetical Protein	0722	(CT654)	CT654 Hypothetical Protein
0399	(CT253)	CT253 Hypothetical Protein	0725	(CT652)	CT652.1 Hypothetical Protein
0400	(CT254)	CT254 Hypothetical Protein	0726	(CT620)	CT620 Hypothetical Protein
0401	(CT255)	CT255 Hypothetical Protein	0727	(CT619)	CT619 Hypothetical Protein
0405	(CT105)	CT105 Hypothetical Protein	0739	(CT638)	CT368 Hypothetical Protein
0408	(CT102)	CT102 Hypothetical Protein	0742	(CT635)	CT635 Hypothetical Protein
0409	(CT260)	CT260 Hypothetical Protein	0746	(CT632)	CT632 Hypothetical Protein
0411	(CT262)	CT262 Hypothetical Protein	0747	(CT631)	CT631 Hypothetical Protein
0412	(CT263)	CT263 Hypothetical Protein	0751	(CT651)	CT651 Hypothetical Protein
0415	(CT266)	CT266 Hypothetical Protein	0755	(CT616)	CT616 Hypothetical Protein
0420	(CT271)	CT271 Hypothetical Protein	0760	(CT611)	CT611 Hypothetical Protein
0422	(CT273)	CT273 Hypothetical Protein	0761	(CT610)	CT610 Hypothetical Protein
0423	(CT274)	CT274 Hypothetical Protein	0764	(CT648)	CT648 Hypothetical Protein
0425	(CT276)	CT276 Hypothetical Proteins	0765	(CT647)	CT647 Hypothetical Protein
0426	(CT277)	CT277 Similarity	0766	(CT646)	CT646 Hypothetical Protein
0434	(CT283)	CT283 Hypothetical Protein	0767	(CT645)	CT645 Hypothetical Protein
0441	(CT007)	CT007 Hypothetical Protein	0770	(CT642)	CT642 Hypothetical Protein
0442	(CT006)	CT006 Hypothetical Protein	0774	(CT606)	CT606.1 Hypothetical Protein
0443	(CT005)	CT005 Hypothetical Protein	0776	(CT605)	CT605 Hypothetical Protein
0474	(CT365)	CT365 Hypothetical Protein	0779	(CT602)	CT602 Hypothetical Protein
0476	(CT865)	CT865 Hypothetical Protein	0783	(CT598)	CT598 Hypothetical Protein
0480	(CT383)	CT383 Hypothetical Protein	0791	(CT590)	CT590 Hypothetical Protein
0485	(CT382)	CT382.1 Hypothetical Protein	0792	(CT589)	CT589 Hypothetical Protein
0487	(CT384)	CT384 Hypothetical Protein	0803	(CT584)	CT584 Hypothetical Protein
0489	(CT386)	CT386 Hypothetical Protein	0807	(CT580)	CT580 Hypothetical Protein
0490	(CT387)	CT387 Hypothetical Protein	0808	(CT579)	CT579 Hypothetical Protein
0491	(CT389)	CT389 Hypothetical Protein	0809	(CT578)	CT578 Hypothetical Protein
0496	(CT391)	CT391 Hypothetical Protein	0810	(CT577)	CT577 Hypothetical Protein
0497	(CT388)	CT388 Hypothetical Protein	0814	(CT573)	CT573 Hypothetical Protein
0506	(CT421)	CT421 Hypothetical Protein	0818	(CT569)	CT569 Hypothetical Protein
0507	(CT421)	CT421.1 Hypothetical Protein	0819	(CT568)	CT568 Hypothetical Protein
0508	(CT421)	CT421.2 Hypothetical Protein	0820	(CT567)	CT567 Hypothetical Protein
0512	(CT425)	CT425 Hypothetical Protein	0821	(CT566)	CT566 Hypothetical Protein
0514	(CT427)	CT427 Hypothetical Protein	0822	(CT565)	CT565 Hypothetical Protein
0518	(CT429)	CT429 Hypothetical Protein	0827	(CT560)	CT560 Hypothetical Protein
0522	(CT433)	CT433 Hypothetical Protein	0834	(CT556)	CT556 Hypothetical Protein
0525	(CT398)	CT398 Hypothetical Protein	0840	(CT700)	CT700 Hypothetical Protein
0533	(CT406)	CT406 Hypothetical Protein	0842	(CT702)	CT702 Hypothetical Protein
0537	(CT814)	CT814.1 Hypothetical Protein	0843	(CT702)	CT702 Hypothetical Protein
0538	(CT814)	CT814 Hypothetical Protein	0852	(CT711)	CT711 Hypothetical Protein
0554	(CT440)	CT440 Hypothetical Protein	0853	(CT712)	CT712 Hypothetical Protein
0559	(CT441)	CT441.1 Hypothetical Protein	0857	(CT716)	CT716 Hypothetical Protein
0565	(CT449)	CT449 Hypothetical Protein	0859	(CT718)	CT718 Hypothetical Protein
0572	(CT456)	CT456 Hypothetical Protein	0865	(CT724)	CT724 Hypothetical Protein
0582	(CT465)	CT465 Hypothetical Protein	0869	(CT728)	CT728 Hypothetical Protein
0583	(CT466)	CT466 Hypothetical Protein	0874	(CT733)	CT733 Hypothetical Protein
0588	(CT469)	CT469 Hypothetical Protein	0875	(CT734)	CT734 Hypothetical Protein
0589	(CT470)	CT470 Hypothetical Protein	0884	(CT741)	CT741 Hypothetical Protein
0590	(CT471)	CT471 Hypothetical Protein	0887	(CT744)	CHLTR Possible Phosphoprotein
0593	(CT474)	CT474 Hypothetical Protein	0896	(CT753)	CT753 Hypothetical Protein
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0648	(CT529)	CT529 Hypothetical Protein	0945	(CT795)	CT795 Hypothetical Protein
0658	(CT538)	CT538 Hypothetical Protein	0956	(CT805)	CT805 Hypothetical Protein
0667	(CT546)	CT546 Hypothetical Protein	0960	(CT809)	CT809 Hypothetical Protein
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0669	(CT548)	CT548 Hypothetical Protein	0994	(CT837)	CT837 Hypothetical Protein
0671	(CT550)	CT550 Hypothetical Protein	0995	(CT838)	CT838 Hypothetical Protein
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0687	(CT482)	CT482 Hypothetical Protein	1005	(CT848)	CT848 Hypothetical Protein
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0700	(CT676)	CT676 Hypothetical Protein	1007	(CT849)	CT849.1 Hypothetical Protein
0705	(CT671)	CT671 Hypothetical Protein	1008	(CT850)	CT850 Hypothetical Protein
0706	(CT670)	CT670 Hypothetical Protein	1010	(CT852)	CT852 Hypothetical Protein

1011	(CT853)	CT853 Hypothetical Protein	0011	0205	0459	1029
1015	(CT857)	CT857 Hypothetical Protein	0012	0209	0460	1040
1016	(CT858)	CT858 Hypothetical Protein	0028	0210	0461	1051
1019	(CT860)	CT860 Hypothetical Protein	0029	0211	0462	1052
1020	(CT861)	CT861 Hypothetical Protein	0034	0212	0463	1053
1022	(CT863)	CT863 Hypothetical Protein	0041	0213	0464	1054
1032	(CT373)	CT373 Hypothetical Protein	0042	0214	0465	1055
1033	(CT372)	CT372 Hypothetical Protein	0043	0215	0472	1056
1034	(CT371)	CT371 Hypothetical Protein	0044	0216	0473	1064
1057	(CT356)	CT356 Hypothetical Protein	0045	0218	0481	1065
1058	(CT355)	CT355 Hypothetical Protein	0046	0220	0483	1066
1061	(CT330)	CT330 Hypothetical Protein	0047	0221	0492	1070
1073	(CT371)	CT371 Hypothetical Protein	0049	0222	0493	1071
Coding Genes Not in <i>C. trachomatis</i>			0050	0223	0494	1072
0486		Hypothetical Proline Permease	0051	0224	0498	
0279		Possible ABC Transporter Permease Protein	0063	0225	0499	
0505		3-Methyladenine DNA Glycosylase	0064	0226	0516	
0193	argR	Similarity to Arginine Repressor	0066	0233	0517	
1041	bioA	Adenosylmethionine-8-Amino-7-Oxononanoate Aminotransferase	0067	0240	0523	
			0069	0241	0524	
1044	bioB	Biotin Synthase	0070	0242	0553	
1042	bioD	Dethiobiotin synthetase	0099	0243	0574	
0585		Similarity to Cps IncA_2	0124	0266	0600	
0562		CHLPS 43 kDa Protein Homolog_1	0125	0267	0656	
0927		CHLPS 43 kDa Protein Homolog_2	0126	0268	0664	
0928		CHLPS 43 kDa Protein Homolog_3	0130	0277	0677	
0929		CHLPS 43 kDa Protein Homolog_4	0131	0283	0678	
1045		Conserved Hypothetical Membrane Protein	0132	0284	0685	
0251		Conserved Hypothetical Protein	0142	0285	0686	
0278		Conserved Outer Membrane Lipoprotein Protein	0146	0287	0724	
0907		CutA-like Periplasmic Divalent Cation Tolerance Protein	0147	0352	0731	
			0155	0353	0745	
0171	guaA	GMP Synthase	0156	0354	0753	
0172	guaB	Inosine 5'-Monophosphate Dehydrogenase	0157	0355	0794	
0608		Uridine 5'-Monophosphate Synthase	0158	0356	0795	
0735		Uridine Kinase	0159	0357	0796	
0980		Similar to <i>Saccharomyces cerevisiae</i> 52.9KDa Protein	0162	0358	0797	
			0163	0365	0798	
0232		Similarity to 5'-Methylthioadenosine Nucleosidase	0164	0366	0799	
1046		Tryptophan Hydroxylase	0165	0367	0829	
0477	yqeV_Bs	Conserved Hypothetical Protein	0166	0368	0830	
0048	yqfF_Bs	Conserved Hypothetical IM Protein	0167	0371	0831	
0587	yvyD_Bs	Conserved Hypothetical Protein	0168	0372	0881	
0143	yxjG_Bs_1	Conserved Hypothetical Protein	0169	0375	0882	
0448	yxjG_Bs_2	Conserved Hypothetical Protein	0170	0376	0913	
0006	0180	0440 0977	0173	0391	0914	
0007	0181	0455 0978	0174	0398	0930	
0008	0190	0456 1018	0175	0404	0944	
0009	0203	0457 1023	0177	0431	0964	
0010	0204	0458 1027	0178	0432	0975	
			0179	0439	0976	


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1: [P38001](#). 50S ribosomal pro...[gi:7404434] [BLink](#), [Domains](#), [Links](#)

LOCUS P38001 130 aa linear BCT 01-OCT-2004

DEFINITION 50S ribosomal protein L7/L12.

ACCESSION P38001

VERSION P38001 GI:7404434

DBSOURCE swissprot: locus RL7_CHLMU, accession P38001;

class: standard.

created: Oct 1, 1994.

sequence updated: May 30, 2000.

annotation updated: Oct 1, 2004.

xrefs: gi: [8163261](#), gi: [7190628](#), gi: [11276725](#)

xrefs (non-sequence databases): HSSPP02392, Siena-2DPAGEP38001,

TIGRTC0590, HAMAPMF_00368, InterProIPR000206, InterProIPR008932,

PfamPF00542, ProDomPD001326, TIGRFAMsTIGR00855

KEYWORDS Complete proteome; Ribosomal protein.

SOURCE Chlamydia muridarum

ORGANISM Chlamydia muridarum

Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.

REFERENCE 1 (residues 1 to 130)

AUTHORS Read,T.D., Brunham,R.C., Shen,C., Gill,S.R., Heidelberg,J.F.,

White,O., Hickey,E.K., Peterson,J., Utterback,T., Berry,K.,

Bass,S., Linher,K., Weidman,J., Khouri,H., Craven,B., Bowman,C.,

Dodson,R., Gwinn,M., Nelson,W., DeBoy,R., Kolonay,J., McClarty,G.,

Salzberg,S.L., Eisen,J. and Fraser,C.M.

TITLE Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39

JOURNAL Nucleic Acids Res. 28 (6), 1397-1406 (2000)

MEDLINE [20150255](#)

PUBMED [10684935](#)

REMARK SEQUENCE FROM N.A.

STRAIN=MoPn / Nigg

REFERENCE 2 (residues 1 to 130)

AUTHORS Engel,J.N., Pollack,J., Malik,F. and Ganem,D.

TITLE Cloning and characterization of RNA polymerase core subunits of Chlamydia trachomatis by using the polymerase chain reaction

JOURNAL J. Bacteriol. 172 (10), 5732-5741 (1990)

MEDLINE [91008945](#)

PUBMED [2211507](#)

REMARK SEQUENCE OF 2-127 FROM N.A.

STRAIN=MoPn

COMMENT On Apr 3, 2000 this sequence version replaced gi:[585891](#).

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 collaboration between the Swiss Institute of Bioinformatics and
 the EMBL outstation - the European Bioinformatics Institute.
 The original entry is available from <http://www.expasy.ch/sprot>
 and <http://www.ebi.ac.uk/sprot>

[FUNCTION] Seems to be the binding site for several of the factors involved in protein synthesis and appears to be essential for accurate translation (By similarity).

[SIMILARITY] Belongs to the L12P family of ribosomal proteins.

FEATURES Location/Qualifiers
source 1..130
 /organism="Chlamydia muridarum"
 /db_xref="taxon:83560"
gene 1..130
 /gene="rplL"
 /locus_tag="TC0590"
Protein 1..130
 /gene="rplL"
 /locus_tag="TC0590"
 /product="50S ribosomal protein L7/L12"
Region 15
 /gene="rplL"
 /locus_tag="TC0590"
 /region_name="Conflict"
 /note="G -> R (in Ref. 2)."
Region 52
 /gene="rplL"
 /locus_tag="TC0590"
 /region_name="Conflict"
 /note="A -> R (in Ref. 2)."
Region 60..128
 /gene="rplL"
 /locus_tag="TC0590"
 /region_name="Ribosomal protein L7/L12 C-terminal domain"
 /note="Ribosomal_L12"
 /db_xref="CDD:1101"

ORIGIN

1 mttsetlv eqlsqgtvle lsqkkmllee kwdvtaaapv vavagaaaag dapasaapte
61 faviledvpa dkkigvkvv revtgalke akemteglpk tvkektksd aedtvkklqe
121 agakavakgl

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